IN THE SPECIFICATION:

Please amend paragraph [0009] as follows:

[0009] In one embodiment, an isolated polypeptide comprising the amino acid sequence Y (Trp/Phe) Xaa_1 Xaa_2 Xaa_3 Xaa_4 Xaa_5 (Trp/Phe) Xaa_6 Xaa_7 (Trp/Phe) Z (SEQ ID NOs:17-20) is provided. Y, which may or may not be present, is a peptidic structure containing at least one cysteine residue and having the formula $(Xaa)_n$. Xaa is any amino acid residue and n is an integer from 1 to 20. Z, which may or may not be present, is a peptidic structure containing at least one cysteine residue and having the formula $(Xaa)_n$, wherein Xaa is any amino acid residue and n is an integer from 1 to 20. The amino acid residues of in Xaa_1 through Xaa_7 can be any amino acid and the amino acid residues of Xaa_1 through Xaa_5 are positively charged.

Please amend paragraph [0010] as follows:

[0010] In another embodiment, an isolated polypeptide comprising the amino acid sequence Y (Trp/Phe) Xaa_1 Xaa_2 Xaa_3 Xaa_4 Xaa_5 (Trp/Phe) Xaa_6 Xaa_7 Xaa_8 (Trp/Phe) Z (SEQ ID NOs:21-24) is provided. Y, which may or may not be present, is a peptidic structure containing at least one cysteine residue and having the formula $(Xaa)_n$. Xaa is any amino acid residue and n is an integer from 1 to 20. Z, which may or may not be present, is a peptidic structure containing at least one cysteine residue and having the formula $(Xaa)_n$, wherein Xaa is any amino acid residue and n is an integer from 1 to 20. The amino acid residues of Xaa_1 through Xaa_8 is any amino acid, and at least two of the residues of Xaa_1 through Xaa_5 are positively charged.

Please amend paragraph [0036] as follows:

[0036] Ala (A) Gly; Ser Arg (R) Lys Asn (N) Gln (SEQ ID NO:25); His Cys (C) Ser Gln (Q) Asn Glu (E) Asp Gly (G) Ala (SEQ ID NO:26); Pro His (H) Asn; Gln-Ile (I) Leu; Val Leu (L) Ile; Val Lys (K) Arg; Gln; Glu Met (M) Leu; Tyr; Ile Phe (F) Met; Leu; Tyr Ser (S) Thr Thr (T) Ser Trp (W) Tyr Tyr (Y) Trp (SEQ ID NO:27); Phe Val (V) Ile; Leu.

Please amend paragraph [0056] as follows:

[0056] The identified sequences had 3-fold more bulky hydrophobic residues (phenylalanine or tryptophan) than did sequences randomly picked from the starting library. Selected sequences shared bulky hydrophobic amino acids that were spaced at even intervals [(W/F)X_5(W/F)$X_{2/3}$(W/F)] ~~(SEQ ID NO:1)~~ (SEQ ID NOs:1 and 33, respectively), and had two positively charged residues (and no negatively charged residues) in the X_5 region.

Please amend paragraph [0069] as follows:

[0069] A cysteine-linked phage peptide library encoding $5X10^7$ random 20 amino acid insertions was obtained. $A\beta_{1-40}$ peptide (DAEFKHDSGTEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV) (SEQ ID NO:28) was purchased from Bachem (Torrence, CA). Biotinylated anti-sheep M13 phage polyclonal antibody was purchased from 5 Prime -3 Prime (Boulder, CO). Alkaline phosphatase and horseradish peroxidase-coupled streptavidin were purchased from Boehringer Mannheim (Indianapolis, IN) and Jackson immunochemicals (West Grove, PA). Radionucleotides for DNA sequencing were purchased from Amersham (Piscataway, NJ). Oligonucleotides were purchased from Genosys (The Woodlands, TX). Recombinant peptides fused to thioredoxin were made and purified using plasmids and reagents in the His-Patch ThioFusion expression

system from Invitrogen (Carlsbad, CA). Anti-Aß monoclonal antibody (2066) was a generous gift from Edward Koo (UC San Diego). Synthetic peptides containing an N-terminal biotin were-synthesized and purified by AnaSpec (San Jose, CA).

Please amend paragraph [0071] as follows:

[0071] *DNA sequencing of phage clones:* At the end of Round 3 of panning, phage-infected K91 cells were diluted and plated as single colonies on LB-Agar plates with 75μg/ml kanamycin. Individual colonies were grown up at 37 C for 12 hours in LB with 1 μg/ml kanamycin. Bacteria were spun down at 10,000g for five minutes, after which the supernatant was precipitated in PEG/NaOAc (3.6%/450 mM) for 24 hours on ice. Precipitated phage DNA was isolated by spinning at 10,000g for 15 minutes and re-suspended in Tris-EDTA (TE, pH 7.5). Anti-phage primer was added (5' gtttgtcgtctttccagacg) (SEQ ID NO:29) and DNA sequencing reactions were run using the Sequenase sequencing kit (Amersham, Piscataway, NJ).

Please amend paragraph [0075] as follows:

[0075] 5' CGGGGTACCT GCAGAATGCG ATTGGGGGAA GGGGGGTCGG TGGCGGTTGT GGCCGGGTGCGTCGGGGAAG ACGGAGGCGT GCGGCCCGCC GTATTAGTCT AGAGC (forward) (SEQ ID NO:30) and

Please amend paragraph [0076] as follows:

[0076] 5' GCTCTAGACTAATACGGCGGGCCGCACGCCTCCGTCTTCCCCGACGC ACCCGGCCACAACCGCCACCGACCCCCCTTCCCCCAATCGCATTCTGCAGGTACC CCG (reverse) (SEQ ID NO:31). This added several flanking amino acids from the phage coat sequence at either end of the 20 amino acid insert, such that the sequence around the

insert site (beginning at the Kpn I site in pHisThioC) was PAEC-insert (DWGKGGRWRLWPGASGKTEA) –CGPPY (SEQ ID NO:32)-stop. XL1-Blue bacteria were transformed with plasmid either containing insert (pThio, Aß) or lacking insert (pThio). Transformed bacteria were grown and protein induced with 1mM IPTG in log phase. Cells were pelleted and harvested by repeated cycles of freezing and thawing with subsequent sonication. Recombinant Thio or Thio-Aß protein was purified by incubation with ProBond nickel chelating resin (Invitrogen; Carlsbad, CA.). Protein was bound with pH 7.8 buffer, washed successively with pH 6.0 and pH 5.5 buffers, and eluted with pH 4.0 buffer according to the manufacturer's instructions. Eluted protein was immediately re-pHed to 7.5 after elution. Recombinant protein comprised ca. 80% of the protein in fractions used for binding studies.